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SEQUENCE LISTING

<110> ABBOTT, Catherine Anne
GORRELL, Mark Douglas

<120> DIPEPTIDYL PEPTIDASES

<130> FCSB-100-Div. 1

<140> 10/825,632

<141> 2004-04-15

<150> US 10/070,464

<151> 2002-07-18

<150> PCT/AU00/01085

<151> 2000-09-11

<150> AU PQ5709

<151> 2000-02-18

<150> AU PQ2762

<151> 1999-09-10

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Asp	Arg	Ile	Tyr	Tyr	Leu	Ala	Met	Ser	Gly	Glu	Asn	Arg	Glu	Asn	Thr
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Pro Asp Trp Ile Ala	Phe Ile His Ser	Asn Asp Ile Trp	Ile Ser Asn	
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Leu Gln Glu Glu Phe	Asp Arg Tyr Ser	Gly Tyr Trp Trp	Cys Pro Lys	
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Ala Glu Thr Thr Pro	Ser Gly Gly Lys	Ile Leu Arg Ile	Leu Tyr Glu	
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Glu Asn Asp Glu Ser	Glu Val Glu Ile	Ile His Val Thr	Ser Pro Met	
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Ala Asn Pro Lys Val	Thr Phe Lys Met	Ser Glu Ile Met	Ile Asp Ala	
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Arg Leu Gln Ile Val	Leu Ile Ser Pro	Glu Leu Phe Ile	Pro Val Glu	
385	390	395	400	
Asp Asp Val Met Glu	Arg Gln Arg Leu	Ile Glu Ser Val	Pro Asp Ser	
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Val Thr Pro Leu Ile	Ile Tyr Glu Glu	Thr Thr Asp Ile	Trp Ile Asn	
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Ile His Asp Ile Phe	His Val Phe Pro	Gln Ser His Glu	Glu Glu Ile	
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Ile Gln Val Asp Glu	Val Arg Arg Leu	Val Tyr Phe Glu	Gly Thr Lys	
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Asp Ser Pro Leu Glu	His His Leu Tyr	Val Val Ser Tyr	Val Asn Pro	
	530	535	540	
Gly Glu Val Thr Arg	Leu Thr Asp Arg	Gly Tyr Ser His	Ser Cys Cys	
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Gln	Asn	Glu	Gln	Gly	Tyr	Tyr	Leu	Gly	Ser	Val	Ala	Met	Gln	Ala	Glu
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Lys	Phe	Pro	Ser	Glu	Pro	Asn	Arg	Leu	Leu	Leu	Leu	His	Gly	Phe	Leu
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Asp	Glu	Asn	Val	His	Phe	Ala	His	Thr	Ser	Ile	Leu	Leu	Ser	Phe	Leu
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Val	Arg	Ala	Gly	Lys	Pro	Tyr	Asp	Leu	Gln	Ile	Tyr	Pro	Gln	Glu	Arg
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His	Ser	Ile	Arg	Val	Pro	Glu	Ser	Gly	Glu	His	Tyr	Glu	Leu	His	Leu
	850					855				860					
Leu	His	Tyr	Leu	Gln	Glu	Asn	Leu	Gly	Ser	Arg	Ile	Ala	Ala	Leu	Lys
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cctaaatt	agccttt	tggtgag	tattcct	gtcagct	aaagct	360
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Ser His Ser Cys Cys Ile Ser Gln His Cys Asp Phe Phe Ile Ser Lys
 35          40          45
Tyr Ser Asn Gln Lys Asn Pro His Cys Val Ser Leu Tyr Lys Leu Ser
 50          55          60
Ser Pro Glu Asp Asp Pro Thr Cys Lys Thr Lys Glu Phe Trp Ala Thr
 65          70          75          80
Ile Leu Asp Ser Ala Gly Pro Leu Pro Asp Tyr Thr Pro Pro Glu Ile
 85          90          95
Phe Ser Phe Glu Ser Thr Thr Gly Phe Thr Leu Tyr Gly Met Leu Tyr
 100         105         110
Lys Pro His Asp Leu Gln Pro Gly Lys Lys Tyr Pro Thr Val Leu Phe
 115         120         125
Ile Tyr Gly Gly Pro Gln Gly Gln Ile Glu Ile Asp Asp Gln Val Glu
 130         135         140
Gly Leu Gln Tyr Leu Ala Ser Arg Tyr Asp Phe Ile Asp Leu Asp Arg
 145         150         155         160
Val Gly Ile His Gly Trp Ser Tyr Gly Gly Tyr Leu Ser Leu Met Ala
 165         170         175
Leu Met Gln Arg Ser Asp Ile Phe Arg Val Ala Ile Ala Gly Ala Pro
 180         185         190
Val Thr Leu Trp Ile Phe Tyr Asp Thr Gly Tyr Thr Glu Arg Tyr Met
 195         200         205
Gly His Pro Asp Gln Asn Glu Gln Gly Tyr Tyr Leu Gly Ser Val Ala
 210         215         220
Met Gln Ala Glu Lys Phe Pro Ser Glu Pro Asn Arg Leu Leu Leu Leu
 225         230         235         240
His Gly Phe Leu Asp Glu Asn Val His Phe Ala His Thr Ser Ile Leu
 245         250         255
Leu Ser Phe Leu Val Arg Ala Gly Lys Pro Tyr Asp Leu Gln Ile Tyr
 260         265         270
Pro Gln Glu Arg His Ser Ile Arg Val Pro Glu Ser Gly Glu His Tyr
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Glu Leu His Leu Leu His Tyr Leu Gln Glu Asn Leu Gly Ser Arg Ile
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<211> 1197

<212> DNA

<213> Homo Sapiens

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<211> 465

<212> PRT

<213> Homo Sapiens

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Gln Pro Phe Glu Ile Leu Phe Glu Gly Val Glu Tyr Ile Ala Arg Ala
35          40          45
Gly Trp Thr Pro Glu Gly Lys Tyr Ala Trp Ser Ile Leu Leu Asp Arg
50          55          60
Ser Gln Thr Arg Leu Gln Ile Val Leu Ile Ser Pro Glu Leu Phe Ile
65          70          75          80
Pro Val Glu Asp Asp Val Met Glu Arg Gln Arg Leu Ile Glu Ser Val
85          90          95
Pro Asp Ser Val Thr Pro Leu Ile Ile Tyr Glu Glu Thr Thr Asp Ile
100         105         110
Trp Ile Asn Ile His Asp Ile Phe His Val Phe Pro Gln Ser His Glu
115         120         125
Glu Glu Ile Glu Phe Ile Phe Ala Ser Glu Cys Lys Thr Gly Phe Arg
130         135         140
His Leu Tyr Lys Ile Thr Ser Ile Leu Lys Glu Ser Lys Tyr Lys Arg
145         150         155         160
Ser Ser Gly Gly Leu Pro Ala Pro Ser Asp Phe Lys Cys Pro Ile Lys
165         170         175
Glu Glu Ile Ala Ile Thr Ser Gly Glu Trp Glu Val Leu Gly Arg His
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Gly Ser Asn Ile Gln Val Asp Glu Val Arg Arg Leu Val Tyr Phe Glu
195         200         205
Gly Thr Lys Asp Ser Pro Leu Glu His His Leu Tyr Val Val Ser Tyr

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210		215		220
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	245	250	255	
Asn Gln Lys Asn Pro	His Cys Val Ser Leu Tyr	Lys Leu Ser Ser Pro		
	260	265	270	
Glu Asp Asp Pro Thr	Cys Lys Thr Lys Glu Phe Trp	Ala Thr Ile Leu		
	275	280	285	
Asp Ser Ala Gly Pro	Leu Pro Asp Tyr Thr Pro	Pro Glu Ile Phe Ser		
	290	295	300	
Phe Glu Ser Thr Thr	Gly Phe Thr Leu Tyr Gly	Met Leu Tyr Lys Pro		
305	310	315	320	
His Asp Leu Gln Pro	Gly Lys Lys Tyr Pro Thr	Val Leu Phe Ile Tyr		
	325	330	335	
Gly Gly Pro Gln Val	Ala Ile Ala Gly Ala	Pro Val Thr Leu Trp	Ile	
	340	345	350	
Phe Tyr Asp Thr Gly	Tyr Thr Glu Arg Tyr Met	Gly His Pro Asp Gln		
	355	360	365	
Asn Glu Gln Gly Tyr	Tyr Leu Gly Ser Val Ala	Met Gln Ala Glu Lys		
	370	375	380	
Phe Pro Ser Glu Pro	Asn Arg Leu Leu Leu Leu	His Gly Phe Leu Asp		
385	390	395	400	
Glu Asn Val His Phe	Ala His Thr Ser Ile Leu	Leu Ser Phe Leu Val		
	405	410	415	
Arg Ala Gly Lys Pro	Tyr Asp Leu Gln Ile Tyr	Pro Gln Glu Arg His		
	420	425	430	
Ser Ile Arg Val Pro	Glu Ser Gly Glu His Tyr	Glu Leu His Leu Leu		
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Ile				
465				

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cgtagtcagt tacgtaaata ctggagaggt gacaaggctg actgaccgtg gctactcaca 720

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<210> 7

<211> 360

<212> PRT

<213> Homo Sapiens

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Thr Pro Ser Gly Gly Lys Ile Leu Arg Ile Leu Tyr Glu Glu Asn Asp
 35          40          45
Glu Ser Glu Val Glu Ile Ile His Val Thr Ser Pro Met Leu Glu Thr
 50          55          60
Arg Arg Ala Asp Ser Phe Arg Tyr Pro Lys Thr Gly Thr Ala Asn Pro
 65          70          75          80
Lys Val Thr Phe Lys Met Ser Glu Ile Met Ile Asp Ala Glu Gly Arg
 85          90          95
Ile Ile Val Asp Glu Val Arg Arg Leu Val Tyr Phe Glu Gly Thr Lys
100          105          110
Asp Ser Pro Leu Glu His His Leu Tyr Val Val Ser Tyr Val Asn Pro
115          120          125
Gly Glu Val Thr Arg Leu Thr Asp Arg Gly Tyr Ser His Ser Cys Cys
130          135          140
Ile Ser Gln His Cys Asp Phe Phe Ile Ser Lys Tyr Ser Asn Gln Lys
145          150          155          160
Asn Pro His Cys Val Ser Leu Tyr Lys Leu Ser Ser Pro Glu Asp Asp
165          170          175
Pro Thr Cys Lys Thr Lys Glu Phe Trp Ala Thr Ile Leu Asp Ser Ala
180          185          190
Gly Pro Leu Pro Asp Tyr Thr Pro Pro Glu Ile Phe Ser Phe Glu Ser
195          200          205
Thr Thr Gly Phe Thr Leu Tyr Gly Met Leu Tyr Lys Pro His Asp Leu
210          215          220
Gln Pro Gly Lys Lys Tyr Pro Thr Val Leu Phe Ile Tyr Gly Gly Pro
225          230          235          240

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Gln	Val	Gln	Leu	Val	Asn	Asn	Arg	Phe	Lys	Gly	Val	Lys	Tyr	Phe	Arg
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Leu	Asn	Thr	Leu	Ala	Ser	Leu	Gly	Tyr	Val	Val	Val	Val	Ile	Asp	Asn
			260					265					270		
Arg	Gly	Ser	Cys	His	Arg	Gly	Leu	Lys	Phe	Glu	Gly	Ala	Phe	Lys	Tyr
		275					280					285			
Lys	Met	Gly	Gln	Ile	Glu	Ile	Asp	Asp	Gln	Val	Glu	Gly	Leu	Gln	Tyr
	290					295					300				
Leu	Ala	Ser	Arg	Tyr	Asp	Phe	Ile	Asp	Leu	Asp	Arg	Val	Gly	Ile	His
305					310					315					320
Gly	Trp	Ser	Tyr	Gly	Gly	Tyr	Leu	Ser	Leu	Met	Ala	Leu	Met	Gln	Arg
				325					330					335	
Ser	Asp	Ile	Phe	Arg	Val	Ala	Ile	Ala	Gly	Ala	Pro	Val	Thr	Leu	Trp
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 tatgttggaa acaaggaggg cagattcatt ccgttattcct aaaacaggta cagcaaattcc 240
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 acattcttgc tgcattcagtc agcactgtga cttctttata agtaagtata gtaaccagaa 480
 gaatccacac tgtgtgtccc tttaacaagc atcaagtcct gaagatgacc caacttgcaa 540
 aacaaaggaa ttttgggcca ccatttttga ttcagcaggc cctcttccctg actatactcc 600
 tccagaaatt ttctcttttg aaagtactac tggatttaca ttgtatggga tgctctacaa 660
 gcctcatgat ctacagcctg gaaagaaata tcctactgtg ctgttcatat atggtgggtcc 720
 tcaggtgcag ttggtgaata atcgggtttaa aggagtcaag tatttccgct tgaataccct 780
 agcctctcta gggttatgtg ttgtagtgat agacaacagg ggatcctgtc accgagggct 840
 taaatttgaa ggcgccttta aatataaaat ggggtcaaata gaaattgacg atcaggtgga 900
 aggactccaa tatctagctt ctcgatatga tttcattgac ttagatcgtg tgggcatcca 960
 cggctgggtcc tatggaggat acctctccct gatggcatta atgcagaggc cagatatctt 1020
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Gln Gly

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<223> PCR primer

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			20					25					30		
Arg	Glu	Asn	Glu	Pro	Ala	Arg	Phe	Glu	Thr	Arg	Ser	Phe	Ser	Gln	Leu
		35					40					45			
Ile	Asp	His	Ala	Arg	Ser	Trp	Lys	Thr	Glu	Val	Arg	Gly	Met	Thr	Thr
	50					55				60					
Gln	Gly	Phe	Thr	Lys	Ile	Ser	Leu	Met	Arg	Ala	Glu	Lys	Asp	Arg	Leu
65					70				75					80	
Asn	Met	Tyr	Ala	Ile	Ser	Ser	Val	Pro	Gly	Thr	Asn	Thr	Gln	Ser	Ile
			85					90					95		
Phe	Ser	Val	Thr	Ile	Pro	Leu	Glu	Leu	Val	Glu	Lys	Ala	Gln	Val	Ala
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Tyr	Ile	Arg	Met	Ser	Cys	Arg	Lys	Thr	Pro	Pro	Ser	Ala	Glu	Phe	Thr
			130				135					140			

Leu	Gln	Cys	Glu	Arg	Gln	Arg	Ser	Gln	Val	Val	Thr	Gly	Ile	Ser	Asp
145					150					155					160
Tyr	Glu	Ile	Arg	Asn	Gly	Lys	Met	Ile	Leu	Met	Ala	Gly	Asp	Gln	Leu
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Phe	Arg	Tyr	Asn	Pro	Leu	Asn	Glu	Ala	Leu	Ala	Ala	Ile	Pro	Ile	Ala
			180					185					190		
Val	Pro	Asp	Asp	Gln	Ser	Ser	Thr	Glu	Pro	Met	Asp	Ile	Ser	Glu	Gly
		195					200					205			
Ser	Ile	Thr	Ser	Gly	Thr	Lys	Gly	Cys	Ser	Asn	Glu	Ala	Pro	Gln	Ser
	210					215					220				
Ser	Thr	Val	Pro	Pro	Val	Thr	Arg	Ile	Pro	Ile	Lys	Lys	Pro	Thr	Thr
225					230					235					240
Ser	Thr	Glu	Lys	Pro	Ala	Thr	Ala	Pro	Pro	Thr	Asn	Asn	Phe	Val	Ser
				245					250						255
Ser	Ala	Lys	Val	Cys	Pro	Ala	Asp	Ser	Ser	Leu	Leu	Ala	Tyr	Val	Leu
			260					265					270		
Asn	Lys	Gln	Val	Tyr	Ile	Glu	Lys	Asn	Gly	Lys	Ile	Ile	His	Arg	Thr
		275					280					285			
Ser	Ser	Asn	Ser	Lys	His	Ile	Thr	Asn	Gly	Val	Pro	Ser	Tyr	Ile	Val
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Gln	Glu	Glu	Leu	Glu	Arg	Phe	Glu	Gly	Ile	Trp	Trp	Ser	Glu	Ser	Lys
305					310					315					320
Thr	Arg	Leu	Leu	Tyr	Glu	His	Val	Asn	Glu	Glu	Lys	Val	Ala	Glu	Ser
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Gln	Phe	Gly	Val	Asn	Gly	Asp	Pro	Pro	Val	Ala	Pro	Met	Lys	Tyr	Pro
			340					345					350		
Arg	Ala	Gly	Thr	Lys	Asn	Ala	Tyr	Ser	Thr	Leu	Arg	Met	Val	Ile	Leu
		355					360					365			
Glu	Asn	Gly	Lys	Ala	Tyr	Asp	Val	Pro	Leu	Lys	Asp	Glu	Val	Ile	Tyr
	370					375					380				
Lys	His	Cys	Pro	Phe	Tyr	Glu	Tyr	Ile	Thr	Arg	Ala	Gly	Phe	Phe	Ser
385					390					395					400
Asp	Gly	Thr	Thr	Val	Trp	Val	Gln	Val	Met	Ser	Arg	Asp	Gln	Ala	Gln
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Cys	Ser	Leu	Leu	Leu	Ile	Pro	Tyr	Thr	Asp	Phe	Leu	Leu	Pro	Glu	Glu
			420					425					430		
Leu	Gly	Gly	Ser	Ile	Lys	Glu	Asp	Asn	Leu	Gln	Leu	Ser	Thr	Asp	Leu
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Asn	Asp	Tyr	Trp	Ile	Asn	Thr	His	Asn	Ala	Ile	Tyr	Pro	Leu	Lys	Ile
				485					490						495
Thr	Asp	Glu	Glu	His	Pro	Met	Tyr	Glu	Phe	Ile	Tyr	Cys	Leu	Glu	Lys
			500					505					510		
Pro	Asn	Gly	Ser	Cys	Leu	Ala	Leu	Ile	Ser	Ala	Glu	Leu	Asp	Gln	Asn
		515					520						525		
Gly	Tyr	Cys	Arg	His	Thr	Glu	Glu	Lys	Leu	Leu	Met	Ala	Glu	Asn	Phe
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Ser	Ile	Asn	Lys	Ser	Met	Gly	Ile	Val	Val	Asp	Glu	Val	Arg	Glu	Leu
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			20					25					30		
Asp	Asp	Ala	Thr	Ala	Asp	Ser	Arg	Lys	Thr	Tyr	Thr	Leu	Thr	Asp	Tyr
		35					40					45			
Leu	Lys	Asn	Thr	Tyr	Arg	Leu	Lys	Leu	Tyr	Ser	Leu	Arg	Trp	Ile	Ser
	50					55					60				
Asp	His	Glu	Tyr	Leu	Tyr	Lys	Gln	Glu	Asn	Asn	Ile	Leu	Val	Phe	Asn
65					70					75					80
Ala	Glu	Tyr	Gly	Asn	Ser	Ser	Val	Phe	Leu	Glu	Asn	Ser	Thr	Phe	Asp
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Glu	Phe	Gly	His	Ser	Ile	Asn	Asp	Tyr	Ser	Ile	Ser	Pro	Asp	Gly	Gln
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Phe	Ile	Leu	Leu	Glu	Tyr	Asn	Tyr	Val	Lys	Gln	Trp	Arg	His	Ser	Tyr
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Thr	Ala	Ser	Tyr	Asp	Ile	Tyr	Asp	Leu	Asn	Lys	Arg	Gln	Leu	Ile	Thr
	130					135					140				
Glu	Glu	Arg	Ile	Pro	Asn	Asn	Thr	Gln	Trp	Val	Thr	Trp	Ser	Pro	Val
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Gly	His	Lys	Leu	Ala	Tyr	Val	Trp	Asn	Asn	Asp	Ile	Tyr	Val	Lys	Ile
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Ile	Ile	Tyr	Asn	Gly	Ile	Thr	Asp	Trp	Val	Tyr	Glu	Glu	Glu	Val	Phe
	195						200					205			
Ser	Ala	Tyr	Ser	Ala	Leu	Trp	Trp	Ser	Pro	Asn	Gly	Thr	Phe	Leu	Ala
	210					215					220				
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225					230					235					240
Tyr	Ser	Asp	Glu	Ser	Leu	Gln	Tyr	Pro	Lys	Thr	Val	Arg	Val	Pro	Tyr
				245					250					255	
Pro	Lys	Ala	Gly	Ala	Val	Asn	Pro	Thr	Val	Lys	Phe	Phe	Val	Val	Asn
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Trp	Ala	Thr	Gln	Glu	Arg	Ile	Ser	Leu	Gln	Trp	Leu	Arg	Arg	Ile	Gln
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Asn	Tyr	Ser	Val	Met	Asp	Ile	Cys	Asp	Tyr	Asp	Glu	Ser	Ser	Gly	Arg
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Trp	Asn	Cys	Leu	Val	Ala	Arg	Gln	His	Ile	Glu	Met	Ser	Thr	Thr	Gly
			340					345					350		
Trp	Val	Gly	Arg	Phe	Arg	Pro	Ser	Glu	Pro	His	Phe	Thr	Leu	Asp	Gly
	355						360					365			
Asn	Ser	Phe	Tyr	Lys	Ile	Ile	Ser	Asn	Glu	Glu	Gly	Tyr	Arg	His	Ile
	370					375					380				
Cys	Tyr	Phe	Gln	Ile	Asp	Lys	Lys	Asp	Cys	Thr	Phe	Ile	Thr	Lys	Gly
385					390					395					400
Thr	Trp	Glu	Val	Ile	Gly	Ile	Glu	Ala	Leu	Thr	Ser	Asp	Tyr	Leu	Tyr

				405					410					415	
Tyr	Ile	Ser	Asn	Glu	Tyr	Lys	Gly	Met	Pro	Gly	Gly	Arg	Asn	Leu	Tyr
			420					425					430		
Lys	Ile	Gln	Leu	Ser	Asp	Tyr	Thr	Lys	Val	Thr	Cys	Leu	Ser	Cys	Glu
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Leu	Asn	Pro	Glu	Arg	Cys	Gln	Tyr	Tyr	Ser	Val	Ser	Phe	Ser	Lys	Glu
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Thr	Leu	His	Ser	Ser	Val	Asn	Asp	Lys	Gly	Leu	Arg	Val	Leu	Glu	Asp
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Asn	Ser	Ala	Leu	Asp	Lys	Met	Leu	Gln	Asn	Val	Gln	Met	Pro	Ser	Lys
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Lys	Leu	Asp	Phe	Ile	Ile	Leu	Asn	Glu	Thr	Lys	Phe	Trp	Tyr	Gln	Met
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Ile	Leu	Pro	Pro	His	Phe	Asp	Lys	Ser	Lys	Lys	Tyr	Pro	Leu	Leu	Leu
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Leu	Asn	Trp	Ala	Thr	Tyr	Leu	Ala	Ser	Thr	Glu	Asn	Ile	Ile	Val	Ala
			565						570					575	
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Ala	Ile	Asn	Arg	Arg	Leu	Gly	Thr	Phe	Glu	Val	Glu	Asp	Gln	Ile	Glu
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Ala	Ala	Arg	Gln	Phe	Ser	Lys	Met	Gly	Phe	Val	Asp	Asn	Lys	Arg	Ile
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Ser	Arg	Trp	Glu	Tyr	Tyr	Asp	Ser	Val	Tyr	Thr	Glu	Arg	Tyr	Met	Gly
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705					710					715					720
Lys	Ala	Leu	Val	Asp	Val	Gly	Val	Asp	Phe	Gln	Ala	Met	Trp	Tyr	Thr
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		740					745					750			
Thr	His	Met	Ser	His	Phe	Ile	Lys	Gln	Cys	Phe	Ser	Leu	Pro		
		755					760					765			